

SEQUENCE LISTING

<110> Gladyshev et al.

<120> MAMMALIAN SELENOPROTEIN DIFFERENTIALLY EXPRESSED IN TUMOR CELLS

<130> 4239-56113

<140> US 09/676,718

<141> 2000-09-28

<150> PCT/US99/07560

<151> 1999-04-06

<150> US 60/080,850

<151> 1998-04-06

<160> 19

<170> PatentIn version 3.1

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<213> Homo sapiens

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<222> (93)..(93)

<223> Xaa is selenocysteine

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Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu 35 40 45

Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp 50 55 60

Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys 70 75 80

Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu Gly 85 90 95

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Phe Arg Gly Leu Gln 115	Ile Lys Tyr 120	Val Arg Gly Ser	Asp Pro Val Leu 125	
Lys Leu Leu Asp Asp 130	Asn Gly Asn 135	Ile Ala Glu Glu 140	Leu Ser Ile Leu	
Lys Trp Asn Thr Asp 145	Ser Val Glu 150	Glu Phe Leu Ser 155	Glu Lys Leu Glu 160	
Arg Ile				
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gag ttt tca tcg gag Glu Phe Ser Ser Glu 35				145
ctt tgc agc tct tgt Leu Cys Ser Ser Cys 50		Gly Gln Phe Asn		193
gat cct gat tgc aga Asp Pro Asp Cys Arg				241

Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys Leu

70 `

Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly

100

115

aaa aag ctg tat gca gga gct att ctt gaa gtt tgt gga tga aaa ttg

gga agg ttc cct caa gtc caa gct ttt gtt agg agt gat aaa ccc aaa

Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys

ctg ttc aga gga ctg caa atc aag tat gtc cgt ggt tca gac cct gta

Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val

ctaaggagtt ggcaagctta acaaaaccca ttttttataa atqtccatcc tcctqcattt

gttgatacca ctaacaaaat gctttgtaac agacttgcgg ttaattatgc aaatgatagt

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cagatgatta ctatgcctca tgtgctgtgt gctctttgaa aggaatgaca gcagactaca

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gtggatcaga tacatacttg gcaaattttt gagttttaca ttcttacaga aaagtccatt

taaaagtgat catttgtaag accaaaatat aaataaaaag tttcaaaaaat c

75

105

120

289

337

385

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95

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Asn Leu Leu Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu
Ala Gln Phe Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val
Cys Gly Xaa Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg
Ser Asp Lys Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg
                85
                                   90
Gly Ser Asp Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala
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Glu Glu Leu Ser Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe
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Leu Ser Glu Lys Leu Glu Arg Ile
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ggg ct Gly Le	eg cgc ttg ctg ctg gcg act gcg ttt caa gcg gtg tct gct ctg eu Arg Leu Leu Ala Thr Ala Phe Gln Ala Val Ser Ala Leu 5 20 25	97
999 90 30	ca gag ttt gcg tca gag gca tgc aga gag ttg ggt ttc tcc agc la Glu Phe Ala Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser 35 40 45	145

•••

aac ttg ctc tgc agc tct tgc gat ctt ctt gga cag ttt aat ctg ctc Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu 50 55 60	193
cca ctg gac cct gtt tgc aga ggg tgc tgt cag gaa gaa gca caa ttt Pro Leu Asp Pro Val Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe 65 70 75	241
gaa acc aaa aag ctg tat gca gga gcc atc ctt gaa gtc tgc gga tga Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly 80 85 90	289
aaa ttg ggg agg ttc cct caa gtc caa gct ttt gtc aga agt gat aaa Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys 95 100 105	337
ccc aaa ctc ttc aga ggt cta cag atc aag tat gtt cga ggc tca gac Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp 110 115 120	385
cct gta cta aag ctt ttg gac gac aac ggg aac att gct gaa gaa cta Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu 125 130 135 140	433
agc atc ctc aaa tgg aac aca gac agt gtg gaa gag ttc ctg agc gag Ser Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu 145 150 155	481
aag ttg gaa cgcatataaa catgcttagt agtttttata ctaatcaaat Lys Leu Glu	530
gaattatcac agcacctaga caataactta gttttgcatg cttacattgg tcatcctttt	590
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tatgtacatc attaatcttc tgacaagaag ctgaagtagc accacagtcc ataatatatc	650
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tatgtacatc attaatcttc tgacaagaag ctgaagtagc accacagtcc ataatatatc aggatctggc aagcttaagg aacccagctc ttagaaattt ctcttcttct acacttgttg ctctcaccag tgaaacgctt tgtaaggagg catctgggta attatgcaaa taagtttgtg ataattgctc cagttctaca aacaacagaa ttttaaatag aggaagtgga taaaggagac acctcccttg ctgtgtgctc tttgaaagta attgacagaa aactacaaac acgtaggatg ccctgcgcct cagcagcacc caccccagag cctcttggcg tgcccagctt tctttcagt acaagtattt gtagttgta atgaatgtgc cacatacagg ttttgtagct tattattatg	650 710 770 830 890 950

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Leu Leu Leu Ala Thr Ala Phe Gln Ala Val Ser Ala Leu Gly Ala Glu 20 25 30

Phe Ala Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu 35 40 45

Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Pro Leu Asp 50 55 60

Pro Val Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys 70 75 80

Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu Gly 85 90 95

Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys Leu 100 105 110

Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val Leu 115 120 125

Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu 130 135 140

Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu 145 150 155 160

Arg Ile

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Gly Glu Val Glu Glu Tyr Lys Ile Asp Val Glu Glu Cys Lys Ala Ala
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                                25
                                                    30
Gly Phe Asn Pro Glu Thr Leu Lys Cys Gly Leu Cys Glu Arg Leu Ser
       35
                            40
Asp Tyr His Leu Glu Thr Leu Leu Thr Asp Cys Leu Gln Cys Cys Ile
    50
                        55
Lys Glu Glu Glu Phe Lys His Glu Lys Tyr Pro Thr Ala Ile Leu Glu
65
                    70
                                        75
Val Cys Glu Cys Asn Leu Ala Arg Phe Pro Gln Val Gln Ala Phe Val
His Lys Asp Met Ala Arg Gln Phe Gly Gly Lys Val Lys Val Lys His
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24

25

105

100

Val Arg Gly Val Arg Pro Gln Val Ala Leu Lys Asp Ala Asp Phe Lys 115 . 120 . 125

Xaa Lys Glu Val Leu Ser Val Glu Lys Trp Asp Thr Asp Thr Leu Ile 130 . 135 . 140

Asp Phe Phe Asn Gln Trp Leu Glu

145 150

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Glu Ile Cys Glu Cys Asn Leu Gly Arg Phe Pro Gln Ala Glu Ala Phe 20 25 30

Val Lys Ser Asn Met Val Lys Lys Trp Gly Thr Cys Val Lys Val His 35 40 45

His Val Arg Gly Thr Leu Pro Thr Ile Lys Leu Leu Asp Ala Gln Gly 50 55 60

Glu Val Gln Lys Thr Met Asn Ile Glu Lys Trp Asp Thr Asp Thr Ile 65 70 75 80

Thr Glu Phe Leu Asn Thr Trp Leu Glu 85

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1 5 10 15

Glu Gly Phe Gly Ala Arg Glu Cys Glu Glu Leu Gly Phe Thr Gly Leu
20 25 30

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	<212> DNA	
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